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1
SEQUENCE LISTING

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<120> A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING, IMAGING AND
TREATING VARIOUS CANCERS

<130> DEX-0172

<140> 09/763,978

<141> 2001-02-28

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<151> 1999-09-01

<150> 60/098,880

<151> 1998-09-02

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<170> PatentIn version 3.1

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11

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12

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 <213> Homo sapien

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 35 40 45

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
 50 55 60

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys
 65 70 75 80

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Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
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Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
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Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser
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Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile
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Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser
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14

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Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385 390 395 400

Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
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Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
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Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
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Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
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Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
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SEQUENCE LISTING

<110> Salceda, Susana
 Sun, Yongming
 Recipon, Herve
 Cafferkey, Robert
 DIADEXUS LLC

<120> A NOVEL METHOD OF DIAGNOSING, MONITORING, STAGING,
 IMAGING AND TREATING VARIOUS CANCERS

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<151> 1998-09-02

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<212> DNA

<213> Homo sapiens

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<210> 3

<211> 1709

<212> DNA

<213> Homo sapiens

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<211> 359
<212> DNA
<213> Homo sapiens
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<213> Homo sapiens
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tctaaatgtt tgccccgcca tccttttcca cagtatcctt cttccctcct cccctgtctc 1020
tggtgtgtct gagcagtcta gaagagtgca tctccagcct atgaaacagc tgggtctttg 1080
gccataagaa gtaaagattt gaagacagaa ggaagaaact caggagtaag cttctagccc 1140
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aactcctgct tgtttttctt ttggccatgg gaaggtttac cagtagaatc cttgctaggt 1260
tgatgtgggc catacattcc ttttaataaac cattgtgtac ataagagggt gctgtgttcc 1320
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<210> 7

<211> 291

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (277)

<400> 7

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gtcttaggtt tcattctcag atgactgggt gaacagcagt gttctttgct aagatgggga 180
agactaggga aaagagccag ttctgtattg agcatattat atttaagaca atcccatctg 240
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<210> 8

<211> 1275

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (410)

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<220>
 <221> unsure
 <222> (728)..(756)

<220>
 <221> unsure
 <222> (957)

<400> 8
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 cttaattatc agcttgaagg tattttttgta ttaaaagtgt acattgaaga acctaagtgg 240
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 aaaaaactaa aattgttaat tacaagaaaa tataggtgct taccttttga aggtttatta 480
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 catttgacat caggggtgtt ataagtactg cacttaatac aaagctattt ctcaatngtg 960
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 tgcaactggg aaataaaaaga caaatgctcc agtttgtctt tctcaacctt tgagttctta 1140
 acctttgagt taaaacctag tctaaatagt gggaatgtct tggtttacag taagggtttc 1200
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 ttttatagat aagtg 1275

<210> 9
 <211> 2479
 <212> DNA
 <213> Homo sapiens

<400> 9
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 cggaaaaccc ctatcccgca cagcccactg tgggtcccccac tgtctacgag gtgcatccgg 180
 ctcagtacta cccgtccccc gtgcccaggt acgccccgag ggtcctgacg caggcttcca 240
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 agaaagcact gtgcatcacc ttgacctgg ggaccttct cgtgggagct gcgctggccg 360
 ctggcctact ctggaagtgc atgggcagca agtgctccaa ctctgggata gagtgcgact 420
 cctcaggtac ctgcatcaac ccctctaact ggtgtgatgg cgtgtcacac tgccccggcg 480
 gggaggacga gaatcggtgt gtgcgctct acggacaaaa cttcatcctt cagatgtact 540
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gggcggcctg cagggacatg ggctataaga ataattttta ctctagccaa ggaatagtgg 660
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<210> 10

<211> 576

<212> DNA

<213> Homo sapiens

<400> 10

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cctgtcacct ggggagtgag aggacaggat agtgcattgt ctttgtctct gaatttttag 180
ttatatgtgc tgtaatgttg ctctgaggaa gcccttgaa agtctatccc aacatatcca 240
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cacttcgcaa ctcagggggc gctgcatttt agtaatgggt caaatgattc actttttatg 360
atgcttccaa aggtgccttg gcttctcttc ccaactgaca aatgccaaag ttgagaaaaa 420
tgatcataat ttttagcataa acagagcagt cggcgacacc gattttataa ataaactgag 480
caccttcttt ttaaacaac aaatgcgggt ttatttctca gatgatgttc atccgtgaat 540

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gggccaggga aggcaccttc accttgacta tatggc

576

<210> 11

<211> 890

<212> DNA

<213> Homo sapiens

<400> 11

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tgaagacaat ttggttacc tcaatgagg agtggaggag gatacagtgc tactaccaac 180
tagtgataa aggccaggga tgcctgctca cctcctacca tgtacaggga cgtctcccca 240
ttacaactac ccaatccgaa gtgtcaactg tgtcaggact aagaaaccct ggttttgagt 300
agaaaagggc ctggaaagag gggagccaac aaatctgtct gcttcctcac attagtcatt 360
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ccaagtctg taagagaaat gcctgagttc tagctcaggt tttcttactc tgaattttaga 600
tctccagacc cttcctggcc acaattcaaa ttaaggcaac aaacatatac cttccatgaa 660
gcacacacag acttttgaaa gcaaggacaa tgactgcttg aattgaggcc ttgaggaatg 720
aagctttgaa ggaaaagaat actttgtttc cagccccctt cccacactct tcatgtgtta 780
accactgctt tcttgagcct tggagccacg gtgactgtat tacatgttgt tatagaaaac 840
tgattttaga gttctgatcg ttcaagagaa tgattaaata tacatttcct 890

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<210> 12

<211> 406

<212> DNA

<213> Homo sapiens

<220>

<221> unsure

<222> (30)

<220>

<221> unsure

<222> (248)

<220>

<221> unsure

<222> (383)

<400> 12

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tccaatacca gctttgagct gaactctgag aatgtgacca tgaaggttgt gtctgtgtc 180
tacaatgtta cgatcaacaa cacatactcc tgtatgattg aaaatgacat tgccaaagca 240
acaggggnta tcaaagtgc agaatcggag atcaaaaggc ggagtcacct acagctgcta 300
aactcaaagg cttctctgtg tgtctcttct ttcttttgcca tcagctgggc acttctgcct 360

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ctcagccctt acctgatgct aanataatgt gccttggcca caaaaa

406

<210> 13

<211> 462

<212> DNA

<213> Homo sapiens

<400> 13

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atggcttccc tggggcagat cctcttctgg agcataatta gcatcatcat tattctggct 120
ggagcaattg cactcatcat tggttttggg atttcaggga gacactccat cacagtcact 180
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catgagttca aagaaggcaa agatgagctg tcggagcagg atgaaatgtt cagaggccgg 360
acagcagtgt ttgctgatca agtgatagtt ggcaatgcct ctttgcggct gaaaaacgtg 420
caactcacag atgctggcac ctacaaatgt tatatcatca ct 462

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<210> 14

<211> 272

<212> DNA

<213> Homo sapiens

<400> 14

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tggggaggcc ctctgctgc cttgggtga caatctcagc tccaggctac agggagaccg 180
ggaggatcac agagccagca tggatcctga cagtgatcaa cctctgaaca gcctcgtcaa 240
ggtgattctg gataaatact acttcctctg cg 272

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<210> 15

<211> 492

<212> PRT

<213> Homo sapiens

<400> 15

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Met Ala Leu Asn Ser Gly Ser Pro Pro Ala Ile Gly Pro Tyr Tyr Glu
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```

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Asn His Gly Tyr Gln Pro Glu Asn Pro Tyr Pro Ala Gln Pro Thr Val
      20             25             30

```

```

Val Pro Thr Val Tyr Glu Val His Pro Ala Gln Tyr Tyr Pro Ser Pro
    35             40             45

```

```

Val Pro Gln Tyr Ala Pro Arg Val Leu Thr Gln Ala Ser Asn Pro Val
    50             55             60

```

```

Val Cys Thr Gln Pro Lys Ser Pro Ser Gly Thr Val Cys Thr Ser Lys

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65		70		75		80									
Thr	Lys	Lys	Ala	Leu	Cys	Ile	Thr	Leu	Thr	Leu	Gly	Thr	Phe	Leu	Val
				85					90					95	
Gly	Ala	Ala	Leu	Ala	Ala	Gly	Leu	Leu	Trp	Lys	Phe	Met	Gly	Ser	Lys
			100					105					110		
Cys	Ser	Asn	Ser	Gly	Ile	Glu	Cys	Asp	Ser	Ser	Gly	Thr	Cys	Ile	Asn
		115					120					125			
Pro	Ser	Asn	Trp	Cys	Asp	Gly	Val	Ser	His	Cys	Pro	Gly	Gly	Glu	Asp
		130				135					140				
Glu	Asn	Arg	Cys	Val	Arg	Leu	Tyr	Gly	Pro	Asn	Phe	Ile	Leu	Gln	Met
145					150					155					160
Tyr	Ser	Ser	Gln	Arg	Lys	Ser	Trp	His	Pro	Val	Cys	Gln	Asp	Asp	Trp
			165						170					175	
Asn	Glu	Asn	Tyr	Gly	Arg	Ala	Ala	Cys	Arg	Asp	Met	Gly	Tyr	Lys	Asn
			180					185					190		
Asn	Phe	Tyr	Ser	Ser	Gln	Gly	Ile	Val	Asp	Asp	Ser	Gly	Ser	Thr	Ser
		195					200					205			
Phe	Met	Lys	Leu	Asn	Thr	Ser	Ala	Gly	Asn	Val	Asp	Ile	Tyr	Lys	Lys
	210					215					220				
Leu	Tyr	His	Ser	Asp	Ala	Cys	Ser	Ser	Lys	Ala	Val	Val	Ser	Leu	Arg
225					230					235					240
Cys	Leu	Ala	Cys	Gly	Val	Asn	Leu	Asn	Ser	Ser	Arg	Gln	Ser	Arg	Ile
				245					250					255	
Val	Gly	Gly	Glu	Ser	Ala	Leu	Pro	Gly	Ala	Trp	Pro	Trp	Gln	Val	Ser
			260					265					270		
Leu	His	Val	Gln	Asn	Val	His	Val	Cys	Gly	Gly	Ser	Ile	Ile	Thr	Pro
		275					280					285			
Glu	Trp	Ile	Val	Thr	Ala	Ala	His	Cys	Val	Glu	Lys	Pro	Leu	Asn	Asn
	290					295					300				
Pro	Trp	His	Trp	Thr	Ala	Phe	Ala	Gly	Ile	Leu	Arg	Gln	Ser	Phe	Met
305					310					315					320
Phe	Tyr	Gly	Ala	Gly	Tyr	Gln	Val	Gln	Lys	Val	Ile	Ser	His	Pro	Asn

325 330 335

Tyr Asp Ser Lys Thr Lys Asn Asn Asp Ile Ala Leu Met Lys Leu Gln
340 345 350

Lys Pro Leu Thr Phe Asn Asp Leu Val Lys Pro Val Cys Leu Pro Asn
355 360 365

Pro Gly Met Met Leu Gln Pro Glu Gln Leu Cys Trp Ile Ser Gly Trp
370 375 380

Gly Ala Thr Glu Glu Lys Gly Lys Thr Ser Glu Val Leu Asn Ala Ala
385 390 395 400

Lys Val Leu Leu Ile Glu Thr Gln Arg Cys Asn Ser Arg Tyr Val Tyr
405 410 415

Asp Asn Leu Ile Thr Pro Ala Met Ile Cys Ala Gly Phe Leu Gln Gly
420 425 430

Asn Val Asp Ser Cys Gln Gly Asp Ser Gly Gly Pro Leu Val Thr Ser
435 440 445

Asn Asn Asn Ile Trp Trp Leu Ile Gly Asp Thr Ser Trp Gly Ser Gly
450 455 460

Cys Ala Lys Ala Tyr Arg Pro Gly Val Tyr Gly Asn Val Met Val Phe
465 470 475 480

Thr Asp Trp Ile Tyr Arg Gln Met Lys Ala Asn Gly
485 490